



## Revision shock in taxonomy

S. BLAIR HEDGES

*Department of Biology, Pennsylvania State University, University Park, PA 16802 USA. E-mail: sbh1@psu.edu*

The current revolution in molecular phylogenetics has led to a large number of revisionary changes in the classification of life in a relatively short period of time. To the non-taxonomist, and to some taxonomists, this might give the illusion of excessive and unnecessary naming of taxa. Vences *et al.* (2013) have made that interpretation, leading them to propose a lengthy and detailed set of criteria—some might call it a mini-ICZN Code—designed to scale back the naming process in taxonomy, hence their title "...economy of change..." Although claimed not to be proposed regulation, it is hard to ignore phrases like "...classifications should avoid deliberately violating any of the three primary [criteria]..." These authors have made some good points, but taxonomists should reject this proposal outright because it is flawed and based on a misunderstanding. If one defines instability as change, any revision will cause temporary instability, by definition. In popular groups of organisms, there may be initial resistance, referred to here as 'revision shock,' but people will eventually get used to new names, lists will get updated, and there will be a new status quo in a few years as the dust settles. This is how it has been since Linnaeus, and it does not require new criteria or regulation.

Vences *et al.* (2013) do not reject all naming of new taxa, and point out that their criteria apply only to cases where naming is optional. However, naming higher taxa in a revision is almost always optional, so their new system would apply to most revisions that name taxa above the species level. No taxonomist would disagree with some criteria listed by Vences *et al.* (2013), such as taxa being monophyletic, or that we should apply our classifications "with care," although the latter phrase, repeated several times, should have gone unstated. Vences *et al.* (2013) go on to present very detailed criteria about methods and statistical analyses that would apply mostly to taxonomists having access to DNA sequences of their organisms. They stress that they have no biases towards individual methods: "by proposing these subcriteria to assess clade stability we do not defend that any kind of data or analytical method is necessarily superior." But a few sentences later they do the opposite and condemn a particular method. "Optimization methods such as, for instance, Maximum Parsimony, Maximum Likelihood, or Bayesian Inference are preferable while phenetic methods such as neighbor-joining must nowadays be considered as insufficient." Although I rarely use neighbor-joining (Saitou & Nei 1987), I am compelled to correct this misleading statement that harks back to debates of long-ago. All of these phylogenetic methods have the desirable quality of minimizing change in the tree, and they usually yield trees that are identical in topology, so there is no need to condemn any one method. Neighbor-joining can correct for complex models of sequence change, is nearly as accurate as maximum likelihood, and is faster than other methods (Tamura *et al.* 2004), which is probably why it is the most widely used phylogenetic method (>18,000 citations per year).

Vences *et al.* (2013) bring up "ease of phenotypic diagnosability" as another criterion in naming higher taxa. This criterion also is problematic, because some morphologically conservative groups will have few diagnostic characters, and those characters will often be difficult to score. Does that make them any less diagnostic? The inference from this criterion is that taxonomic subdivision (naming) should not be done if the original, more inclusive, group is easier to diagnose. But this is normally the case, because diagnosability tends to increase with more inclusivity. Hence, a frog (Order Anura) is more easy to identify than a family of frog, which in turn is more easy to identify than a genus of frog. Everyone knows a bird when they see one, but they may not know the genus of bird. Applying this criterion strictly would give us one genus for all of life. In any case, ease of diagnosability also is in the eye of the beholder, and is thus subjective. Vences *et al.* (2013) qualify this criterion by admitting that molecular characters alone might be justified as diagnostic characters for some cryptic groups of organisms. But this qualification obviates the criterion, because there is no objective definition for a "cryptic" group. Moreover, if molecular characters were acceptable for diagnosing taxa in one group of organisms, why wouldn't they be satisfactory for all?

Subgenera are promoted by Vences *et al.* (2013) because they are invisible when only the binomial is used. Although I have described subgenera and advocated their usage in the past, I have discovered over subsequent years that they can be cumbersome to use in taxonomic and non-taxonomic contexts. When discussing subgenera, their rank must be